



SEQUENCE LISTING

ATTACHMENT

C7
<110> BENAROUS, Richard
MARGOTTIN, Florence
DURAND, Hervé
ARENZANA SEISDEDOS, Fernando
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CONDORCET, Jean-Paul

<120> Human beta-TrCP protein

<130> 935.38812X00

<140> US/09/601,168

<141> 2000-07-28

<150> PCT/FR99/00196

<151> 1999-01-29

<150> FR98 01100

<151> 1998-01-30

<150> FR98 15545

<151> 1998-12-09

<160> 9

<170> PatentIn Ver. 2.1 and manually

<210> 1

<211> 2151

<212> DNA

<213> Artificial sequence

<220>

<221> CDS

<222> (70)..(1776)

<220>

<223> Description of the artificial sequence : cDNA
coding for human beta-TrCP protein

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tcggcgatt atg gac ccg gcc gag gcg gtg ctg caa gag aag gca ctc aag 111
Met Asp Pro Ala Glu Ala Val Leu Gln Glu Lys Ala Leu Lys
1 5 10

ttt atg aat tcc tca gag aga gaa gac tgt aat aat ggc gaa ccc cct 159
Phe Met Asn Ser Ser Glu Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro
15 20 25 30

agg aag ata ata cca gag aag aat tca ctt aga cag aca tac aac agc 207
Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser
35 40 45

tgt gcc aga ctc tgc tta aac caa gaa aca gta tgt tta gca agc act 255
Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser Thr
50 55 60

gct atg aag act gag aat tgt gtg gcc aaa aca aaa ctt gcc aat ggc 303
Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn Gly
65 70 75

act tcc agt atg att gtg ccc aag caa cgg aaa ctc tca gca agc tat 351
Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr
80 85 90

gaa aag gaa aag gaa ctg tgt gtc aaa tac ttt gag cag tgg tca gag 399

Glu 95	Lys	Glu	Lys	Glu	Leu 100	Cys	Val	Lys	Tyr	Phe 105	Glu	Gln	Trp	Ser	Glu 110	
tca Ser	gat Asp	caa Gln	gtg Val	gaa Glu 115	ttt Phe	gtg Val	gaa Glu	cat His	ctt Leu 120	ata Ile	tcc Ser	caa Gln	atg Met	tgt Cys 125	cat His	447
tac Tyr	caa Gln	cat His	ggg Gly 130	cac His	ata Ile	aac Asn	tcg Ser	tat Tyr 135	ctt Leu	aaa Lys	cct Pro	atg Met	ttg Leu 140	cag Gln	aga Arg	495
gat Asp	ttc Phe	ata Ile 145	act Thr	gct Ala	ctg Leu	cca Pro	gct Ala 150	cgg Arg	gga Gly	ttg Leu	gat Asp	cat His 155	atc Ile	gct Ala	gag Glu	543
aac Asn	att Ile 160	ctg Leu	tca Ser	tac Tyr	ctg Leu	gat Asp 165	gcc Ala	aaa Lys	tca Ser	cta Leu	tgt Cys 170	gct Ala	gct Ala	gaa Glu	ctt Leu	591
gtg Val 175	tgc Cys	aag Lys	gaa Glu	tgg Trp	tac Tyr 180	cga Arg	gtg Val	acc Thr	tct Ser	gat Asp 185	ggc Gly	atg Met	ctg Leu	tgg Trp	aag Lys 190	639
aag Lys	ctt Leu	atc Ile	gag Glu	aga Arg 195	atg Met	gtc Val	agg Arg	aca Thr	gat Asp 200	tct Ser	ctg Leu	tgg Trp	aga Arg	ggc Gly 205	ctg Leu	687
gca Ala	gaa Glu	cga Arg	aga Arg 210	gga Gly	tgg Trp	gga Gly	cag Gln	tat Tyr 215	tta Leu	ttc Phe	aaa Lys	aac Asn	aaa Lys 220	cct Pro	cct Pro	735
gac Asp	ggg Gly	aat Asn 225	gct Ala	cct Pro	ccc Pro	aac Asn	tct Ser 230	ttt Phe	tat Tyr	aga Arg	gca Ala	ctt Leu 235	tat Tyr	cct Pro	aaa Lys	783
att Ile 240	ata Ile	caa Gln	gac Asp	att Ile	gag Glu	aca Thr 245	ata Ile	gaa Glu	tct Ser	aat Asn	tgg Trp 250	aga Arg	tgt Cys	gga Gly	aga Arg	831
cat His 255	agt Ser	tta Leu	cag Gln	aga Arg	att Ile 260	cac His	tgc Cys	cga Arg	agt Ser	gaa Glu 265	aca Thr	agc Ser	aaa Lys	gga Gly	gtt Val 270	879
tac Tyr	tgt Cys	tta Leu	cag Gln	tat Tyr 275	gat Asp	gat Asp	cag Gln	aaa Lys	ata Ile 280	gta Val	agc Ser	ggc Gly	ctt Leu	cga Arg 285	gac Asp	927
aac Asn	aca Thr	atc Ile	aag Lys 290	atc Ile	tgg Trp	gat Asp	aaa Lys	aac Asn 295	aca Thr	ttg Leu	gaa Glu	tgc Cys	aag Lys 300	cga Arg	att Ile	975
ctc Leu	aca Thr	ggc Gly 305	cat His	aca Thr	ggt Gly	tca Ser	gtc Val 310	ctc Leu	tgt Cys	ctc Leu	cag Gln	tat Tyr 315	gat Asp	gag Glu	aga Arg	1023
gtg Val 320	atc Ile	ata Ile	aca Thr	gga Gly	tca Ser	tcg Ser 325	gat Asp	tcc Ser	acg Thr	gtc Val	aga Arg 330	gtg Val	tgg Trp	gat Asp	gta Val	1071
aat Asn 335	aca Thr	ggt Gly	gaa Glu	atg Met	cta Leu 340	aac Asn	acg Thr	ttg Leu	att Ile	cac His 345	cat His	tgt Cys	gaa Glu	gca Ala	gtt Val 350	1119
ctg Leu	cac His	ttg Leu	cgt Arg	ttc Phe 355	aat Asn	aat Asn	ggc Gly	atg Met	atg Met 360	gtg Val	acc Thr	tgc Cys	tcc Ser	aaa Lys 365	gat Asp	1167
cgt	tcc	att	gct	gta	tgg	gat	atg	gcc	tcc	cca	act	gac	att	acc	ctc	1215

Arg	Ser	Ile	Ala	Val	Trp	Asp	Met	Ala	Ser	Pro	Thr	Asp	Ile	Thr	Leu	
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cgg	agg	gtg	ctg	gtc	gga	cac	cga	gct	gct	gtc	aat	gtt	gta	gac	ttt	1263
Arg	Arg	Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn	Val	Val	Asp	Phe	
		385					390					395				
gat	gac	aag	tac	att	gtt	tct	gca	tct	ggg	gat	aga	act	ata	aag	gta	1311
Asp	Asp	Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg	Thr	Ile	Lys	Val	
		400				405					410					
tgg	aac	aca	agt	act	tgt	gaa	ttt	gta	agg	acc	tta	aat	gga	cac	aaa	1359
Trp	Asn	Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu	Asn	Gly	His	Lys	
					420					425					430	
cga	ggc	att	gcc	tgt	ttg	cag	tac	agg	gac	agg	ctg	gta	gtg	agt	ggc	1407
Arg	Gly	Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu	Val	Val	Ser	Gly	
				435					440					445		
tca	tct	gac	aac	act	atc	aga	tta	tgg	gac	ata	gaa	tgt	ggg	gca	tgt	1455
Ser	Ser	Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu	Cys	Gly	Ala	Cys	
			450					455					460			
tta	cga	gtg	tta	gaa	ggc	cat	gag	gaa	ttg	gtg	cgt	tgt	att	cga	ttt	1503
Leu	Arg	Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg	Cys	Ile	Arg	Phe	
		465					470					475				
gat	aac	aag	agg	ata	gtc	agt	ggg	gcc	tat	gat	gga	aaa	att	aaa	gtg	1551
Asp	Asn	Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly	Lys	Ile	Lys	Val	
		480				485					490					
tgg	gat	ctt	gtg	gct	gct	ttg	gac	ccc	cgt	gct	cct	gca	ggg	aca	ctc	1599
Trp	Asp	Leu	Val	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro	Ala	Gly	Thr	Leu	
				500						505					510	
tgt	cta	cgg	acc	ctt	gtg	gag	cat	tcc	gga	aga	gtt	ttt	cga	cta	cag	1647
Cys	Leu	Arg	Thr	Leu	Val	Glu	His	Ser	Gly	Arg	Val	Phe	Arg	Leu	Gln	
				515					520					525		
ttt	gat	gaa	ttc	cag	att	gtc	agt	agt	tca	cat	gat	gac	aca	atc	ctc	1695
Phe	Asp	Glu	Phe	Gln	Ile	Val	Ser	Ser	Ser	His	Asp	Asp	Thr	Ile	Leu	
			530					535					540			
atc	tgg	gac	ttc	cta	aat	gat	cca	gct	gcc	caa	gct	gaa	ccc	ccc	cgt	1743
Ile	Trp	Asp	Phe	Leu	Asn	Asp	Pro	Ala	Ala	Gln	Ala	Glu	Pro	Pro	Arg	
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tcc	cct	tct	cga	aca	tac	acc	tac	atc	tcc	aga	taaataacca				tacactgacc	1796
Ser	Pro	Ser	Arg	Thr	Tyr	Thr	Tyr	Ile	Ser	Arg						
		560				565										

tcatacttgc	ccaggaccca	ttaaagttgc	ggtattttaac	gtatctgcca	ataccaggat	1856
gagcaacaac	agtaacaatc	aaactactgc	ccagtttccc	tgtagtagcc	gaggagcagg	1916
gctttgagac	tcctgttggg	acacagttgg	tctgcagtcg	gccaggacg	gtctactcag	1976
cacaactgac	tgcttcagtg	ctgctatcag	aagatgtctt	ctatcaattg	tgaatgattg	2036
gaacttttaa	acctcccctc	ctctcctcct	ttcacctctg	cacctagttt	tttcccattg	2096
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<211> 569

<212> PRT

<213> Artificial sequence

<220>

<223> Description of the artificial sequence : cDNA

coding for human beta-TrCP protein

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			20					25					30		
Ile	Ile	Pro	Glu	Lys	Asn	Ser	Leu	Arg	Gln	Thr	Tyr	Asn	Ser	Cys	Ala
		35					40					45			
Arg	Leu	Cys	Leu	Asn	Gln	Glu	Thr	Val	Cys	Leu	Ala	Ser	Thr	Ala	Met
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Lys	Thr	Glu	Asn	Cys	Val	Ala	Lys	Thr	Lys	Leu	Ala	Asn	Gly	Thr	Ser
65					70					75					80
Ser	Met	Ile	Val	Pro	Lys	Gln	Arg	Lys	Leu	Ser	Ala	Ser	Tyr	Glu	Lys
				85					90					95	
Glu	Lys	Glu	Leu	Cys	Val	Lys	Tyr	Phe	Glu	Gln	Trp	Ser	Glu	Ser	Asp
			100					105					110		
Gln	Val	Glu	Phe	Val	Glu	His	Leu	Ile	Ser	Gln	Met	Cys	His	Tyr	Gln
		115					120					125			
His	Gly	His	Ile	Asn	Ser	Tyr	Leu	Lys	Pro	Met	Leu	Gln	Arg	Asp	Phe
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Ile	Thr	Ala	Leu	Pro	Ala	Arg	Gly	Leu	Asp	His	Ile	Ala	Glu	Asn	Ile
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Leu	Ser	Tyr	Leu	Asp	Ala	Lys	Ser	Leu	Cys	Ala	Ala	Glu	Leu	Val	Cys
				165					170					175	
Lys	Glu	Trp	Tyr	Arg	Val	Thr	Ser	Asp	Gly	Met	Leu	Trp	Lys	Lys	Leu
			180					185					190		
Ile	Glu	Arg	Met	Val	Arg	Thr	Asp	Ser	Leu	Trp	Arg	Gly	Leu	Ala	Glu
		195					200					205			
Arg	Arg	Gly	Trp	Gly	Gln	Tyr	Leu	Phe	Lys	Asn	Lys	Pro	Pro	Asp	Gly
	210					215					220				
Asn	Ala	Pro	Pro	Asn	Ser	Phe	Tyr	Arg	Ala	Leu	Tyr	Pro	Lys	Ile	Ile
225					230					235					240
Gln	Asp	Ile	Glu	Thr	Ile	Glu	Ser	Asn	Trp	Arg	Cys	Gly	Arg	His	Ser
				245					250					255	
Leu	Gln	Arg	Ile	His	Cys	Arg	Ser	Glu	Thr	Ser	Lys	Gly	Val	Tyr	Cys
			260					265					270		
Leu	Gln	Tyr	Asp	Asp	Gln	Lys	Ile	Val	Ser	Gly	Leu	Arg	Asp	Asn	Thr
		275					280					285			
Ile	Lys	Ile	Trp	Asp	Lys	Asn	Thr	Leu	Glu	Cys	Lys	Arg	Ile	Leu	Thr
	290					295					300				
Gly	His	Thr	Gly	Ser	Val	Leu	Cys	Leu	Gln	Tyr	Asp	Glu	Arg	Val	Ile
305					310					315					320
Ile	Thr	Gly	Ser	Ser	Asp	Ser	Thr	Val	Arg	Val	Trp	Asp	Val	Asn	Thr
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Gly	Glu	Met	Leu	Asn	Thr	Leu	Ile	His	His	Cys	Glu	Ala	Val	Leu	His

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		355					360					365									
Ile	Ala	Val	Trp	Asp	Met	Ala	Ser	Pro	Thr	Asp	Ile	Thr	Leu	Arg	Arg						
	370					375					380										
Val	Leu	Val	Gly	His	Arg	Ala	Ala	Val	Asn	Val	Val	Asp	Phe	Asp	Asp						
	385				390					395					400						
Lys	Tyr	Ile	Val	Ser	Ala	Ser	Gly	Asp	Arg	Thr	Ile	Lys	Val	Trp	Asn						
				405					410					415							
Thr	Ser	Thr	Cys	Glu	Phe	Val	Arg	Thr	Leu	Asn	Gly	His	Lys	Arg	Gly						
			420					425					430								
Ile	Ala	Cys	Leu	Gln	Tyr	Arg	Asp	Arg	Leu	Val	Val	Ser	Gly	Ser	Ser						
		435					440					445									
Asp	Asn	Thr	Ile	Arg	Leu	Trp	Asp	Ile	Glu	Cys	Gly	Ala	Cys	Leu	Arg						
	450					455					460										
Val	Leu	Glu	Gly	His	Glu	Glu	Leu	Val	Arg	Cys	Ile	Arg	Phe	Asp	Asn						
	465				470					475					480						
Lys	Arg	Ile	Val	Ser	Gly	Ala	Tyr	Asp	Gly	Lys	Ile	Lys	Val	Trp	Asp						
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Leu	Val	Ala	Ala	Leu	Asp	Pro	Arg	Ala	Pro	Ala	Gly	Thr	Leu	Cys	Leu						
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Arg	Thr	Leu	Val	Glu	His	Ser	Gly	Arg	Val	Phe	Arg	Leu	Gln	Phe	Asp						
		515					520					525									
Glu	Phe	Gln	Ile	Val	Ser	Ser	Ser	His	Asp	Asp	Thr	Ile	Leu	Ile	Trp						
	530					535					540										
Asp	Phe	Leu	Asn	Asp	Pro	Ala	Ala	Gln	Ala	Glu	Pro	Pro	Arg	Ser	Pro						
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Ser	Arg	Thr	Tyr	Thr	Tyr	Ile	Ser	Arg													
				565																	

<210> 3
 <211> 19
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence : sense primer

<400> 3
 ccaaactgcg tataacgcg

19

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Description of the artificial sequence : antisense primer

<400> 4
 ggtgaatcaa cgtgtttagc

20

<210> 5

<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence : sense primer

<400> 5
ggatgatgta tataactatc 20

<210> 6
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence : antisense primer

<400> 6
tttatcccag atcttgattg tgttg 25

<210> 7
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence : primer

<400> 7
ccaggatcct tataacaacat tgacagcagc 30

<210> 8
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence : primer

<400> 8
ccaggatcct tagtcccaga tgaggattg 29

<210> 9
<211> 6
<212> PRT
<213> Unknown organism

<220>
<221> Variant
<222> 4 - 5
<223> Xaa is any natural amino acid

<220>
<221> Phosphorylation
<222> 2 and 6
<223> Serines are phosphorylated

<220>
<223> Description of artificial sequence, consensus sequence

<400> 9
Asp Ser Gly Xaa Xaa Ser